

SEQUENCE LISTING

<110> Zavada, Jan
 Pastorekova, Silvia
 Pastorek, Jaromir

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<130> D-0021.5 PCT

<140> PCT/US99/24879

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<210> 6
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<212> PRT
<213> HUMAN

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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
      20             25             30

Met Pro Val His Pro
      35

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<210> 7
<211> 25
<212> DNA
<213> HUMAN

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<210> 8
<211> 26
<212> DNA
<213> HUMAN

<400> 8
ctctaacttc agggagccct cttctt

26

<210> 9
<211> 48
<212> DNA
<213> HUMAN

<220>
<221> primer_bind
<222> (1)..(48)
<223> anchor primer that anneals to the homopolymeric tail.

<220>
<221> inosine
<222> (36)..(37) (41)..(42) (46)..(47)
<223> each of the modified_bases at positions (36), (37), (41), (42), (46)
and (47) are inosine

<400> 9
cuacuacuac uaggccacgc gtcgactagt acgggaaggg aagggaag

48

<210> 10
<211> 6
<212> PRT
<213> HUMAN

<400> 10
Glu Glu Asp Leu Pro Ser
1 5

<210> 11
<211> 6
<212> PRT
<213> HUMAN

<400> 11

Gly Glu Asp Asp Pro Leu
1 5

<210> 12
<211> 21
<212> PRT
<213> HUMAN

<400> 12
Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg
1 5 10 15

Tyr Gly Gly Asp Pro
20

<210> 13
<211> 16
<212> PRT
<213> HUMAN

<400> 13
His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly
1 5 10 15

<210> 14
<211> 24
<212> PRT
<213> HUMAN

<400> 14
Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu
1 5 10 15

Pro Gly Glu Glu Asp Leu Pro Gly
20

<210> 15
<211> 13
<212> PRT
<213> HUMAN

<400> 15

Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln
 1 5 10

<210> 16
 <211> 16
 <212> PRT
 <213> HUMAN

<400> 16
 Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
 1 5 10 15

<210> 17
 <211> 45
 <212> DNA
 <213> HUMAN

<400> 17
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<210> 18
 <211> 43
 <212> DNA
 <213> HUMAN

<400> 18
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<210> 19
 <211> 10
 <212> DNA
 <213> HUMAN

<400> 19
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<210> 20
 <211> 10
 <212> DNA
 <213> HUMAN

<400> 20
ccacccccat

10

<210> 21
<211> 205
<212> DNA
<213> HUMAN

<400> 21
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cccctccagg cttgctcctc ccccaccag ctctcgtttc caatgcacgt acagcccgta 180
cacaccgtgt gctgggacac cccac 205

<210> 22
<211> 8
<212> PRT
<213> HUMAN

<400> 22
Leu Glu His His His His His His
1 5

<210> 23
<211> 10
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(10)

<400> 23
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10

<210> 24
<211> 10
<212> DNA
<213> HUMAN

<300>
<301> Locker and Buzard,

<303> DNA Sequencing and Mapping

<304> 1

<306> 3-11

<307> 1990

<400> 24

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10

<210> 25

<211> 4

<212> PRT

<213> HUMAN

<220>

<221> SITE

<222> (1)..(4)

<223> sequence element defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989) as motif frequently found in gene regulatory proteins.

<220>

<221> VARIANTS

<222> (3)..(4)

<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989) as motif frequently found in gene regulatory proteins.

<400> 25

Ser Pro Xaa Xaa

1

<210> 26

<211> 4

<212> PRT

<213> HUMAN

<220>

<221> SITE

<222> (1)..(4)

<223> sequence element defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989) as a motif frequently found in gene regulatory proteins.

<220>

<221> VARIANTS

<222> (3)..(4)
 <223> variants in sequence element defined by Suzuki, J. Mol. Biol.,
207: 61-84 (1989) as a motif frequently found in gene
 regulatory proteins.

<400> 26
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 1

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 <211> 540
 <212> DNA
 <213> HUMAN

<220>
 <221> promoter
 <222> (1)..(540)

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 acatgagctg ctttccctct cagccagagg acatgggggg ccccagctcc cctgcctttc 180
 cccttctgtg cctggagctg ggaagcaggc caggggttagc tgaggctggc tggcaagcag 240
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 ccatggcccc gataaccttc tgctgtgca cacacctgcc cctcactcca cccccatcct 360
 agctttggta tgggggagag ggcacagggc cagacaaacc tgtgagactt tggctccatc 420
 tctgcaaaag ggcgctctgt gagtcagcct gctcccctcc aggcttgctc ctccccacc 480
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<210> 28
 <211> 445
 <212> DNA
 <213> HUMAN

<220>
 <221> exon
 <222> (1)
 <223> 1st MN exon

<400> 28
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 ctgtcactgc tgcttctggt gcctgtccat ccccagaggt tgccccggat gcaggaggat 180
 tcccccttgg gaggaggctc ttctggggaa gatgaccac tgggcgagga ggatctgccc 240

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agtgaagagg attcaccag agaggaggat ccacccggag aggaggatct acctggagag 300
gaggatctac ctggagagga ggatctacct gaagttaagc ctaaatacaga agaagagggc 360
tcctgaagt tagaggatct acctactgtt gaggctcctg gagatcctca agaaccacag 420
aataatgcc acaggacaa agaag                                     445

```

```

<210> 29
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<212> DNA
<213> HUMAN

```

```

<220>
<221> exon
<222> (1)
<223> 2nd MN exon

```

```

<400> 29
gggatgacca gagtcattgg cgctatggag                                     30

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```

<210> 30
<211> 171
<212> DNA
<213> HUMAN

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<220>
<221> exon
<222> (1)
<223> 3rd MN exon

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<400> 30
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tcagctccc gccgctccca gaactgcgcc tgcgcaacaa tggccacagt g          171

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<210> 31
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<220>
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<223> 4th MN exon

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 aaggccaccg tttccctgcc gag 143

<210> 32
 <211> 93
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 <213> HUMAN

<220>
 <221> exon
 <222> (1)
 <223> 5th MN exon

<400> 32
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<210> 33
 <211> 67
 <212> DNA
 <213> HUMAN

<220>
 <221> exon
 <222> (1)
 <223> 6th MN exon

<400> 33
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 gaggaag 67

<210> 34
 <211> 158
 <212> DNA
 <213> HUMAN

<220>
 <221> exon
 <222> (1)
 <223> 7th MN exon

<400> 34
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gctacttcca atatgagggg tctctgacta caccgccctg tgcccagggg gtcactctgga 120
ctgtgtttta ccagacagtg atgctgagtg ctaagcag 158

<210> 35
<211> 145
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 8th MN exon

<400> 35
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agcagtcctc gggctgctga gccag 145

<210> 36
<211> 27
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 9th MN exon

<400> 36
tccagctgaa ttctgcctg gctgctg 27

<210> 37
<211> 82
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 10th MN exon

<400> 37
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 tgcagatgag aaggcagcac ag 82

<210> 38
 <211> 191
 <212> DNA
 <213> HUMAN

<220>
 <221> exon
 <222> (1)
 <223> 11th MN exon

<400> 38
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 atatttataa t 191

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 <213> HUMAN

<220>
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 <222> (1)..(1174)
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 tggagagaaa ataaaaaggg tgcaaaaagga gagaggtgag ctggatgaga tgggagagaa 240
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tcctgtaagg  catctgCGtt  tgtgacatcg  ttttggtCGc  caggaaggga  ttggggctct  1140
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<210> 40
<211> 193
<212> DNA
<213> HUMAN

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<220>
<221> intron
<222> (1)..(193)
<223> 2nd MN intron

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<400> 40
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cacTTTTtct  accCGggTtc  cctaagttcc  tgacctaggc  gtcagacttc  ctactatac  180
tctcccaccc  cag                                     193

```

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<210> 41
<211> 131
<212> DNA
<213> HUMAN

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<220>
<221> intron
<222> (1)..(131)
<223> 3rd MN intron

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<400> 41
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gcgcagtGCC  tgcccCGgggg  ttgggctggc  cctaccgggc  ggggCCggct  cacttgcctc  120
tccctacgca  g                                     131

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<210> 42
<211> 89
<212> DNA
<213> HUMAN

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<220>
 <221> intron
 <222> (1)..(89)
 <223> 4th MN intron

<400> 42
 gtgagcgcgg actggccgag aaggggcaaa ggagcggggc ggacgggggc cagagacgtg 60
 gccctctcct accctcgtgt cctttttcag 89

<210> 43
 <211> 1400
 <212> DNA
 <213> HUMAN

<220>
 <221> intron
 <222> (1)..(1400)
 <223> 5th MN intron

<400> 43
 gtaccagatc ctggacaccc cctactcccc gctttcccat cccatgctcc tcccggactc 60
 tatcgtggag ccagagaccc catcccagca agctcactca ggcccctggc tgacaaactc 120
 attcacgcac tgtttggtca tttaacaccc actgtgaacc aggcaccagc cccaacaag 180
 gattctgaag ctgtaggtcc ttgcctctaa ggagcccaca gccagtgggg gaggtgaca 240
 tgacagacac ataggaagga catagtaaag atggtggtca cagaggaggt gacacttaaa 300
 gccttcactg gtagaaaaga aaaggaggtg ttcattgcag aggaaacaga atgtgcaaag 360
 actcagaata tggcctattht aggggaatggc tacatacacc atgattagag gagggcccagt 420
 aaaggggaagg gatggtgaga tgccctgctag gttcactcac tcaacttttat ttattttattht 480
 attttttttga cagtctctct gtgcgccagg ctggagtga gtggtgtgat cttgggtcac 540
 tgcaacttcc gcctcccggg ttcaagggat tctcctgcct cagcttcctg agtagctggg 600
 gttacaggtg tgtgccacca tgcccagcta attttttttt gtatttttag tagacagggg 660
 ttcaccatgt tggtcaggct ggtctcaaac tcttgccctc aagtgatccg cctgactcag 720
 cctaccaaag tgctgattac aagtgtgagc caccgtgccc agccacactc actgattctt 780
 taatgccagc cacacagcac aaagttcaga gaaatgcctc catcatagca tgtcaatatg 840
 ttcatactct taggttcatg atgtttctta cattaggttc ataagcaaaa taagaaaaaa 900
 gaataataaa taaaagaagt ggcattgtcag gacctcacct gaaaagccaa acacagaatc 960
 atgaagggtga atgcagaggt gacaccaaca caaagggtga tatatgggtt cctgtgggga 1020
 gtatgtacgg aggcagcagt gagtgagact gcaaacgtca gaagggcacg ggtcactgag 1080
 agcctagtat cctagtaaag tgggctctct ccctctctct ccagcttgct attgaaaacc 1140
 agtccaccaa gcttggttgg tgcacacagca agagtacata gagtttgaaa taatacatag 1200
 gattttaaga gggagacact gtctctaaaa aaaaaaacia cagcaacaac aaaaagcaac 1260
 aaccattaca attttatggt ccctcagcat tctcagagct gaggaatggg agaggactat 1320
 gggaaccccc ttcattgttc ggccttcagc catggccctg gatacatgca ctcatctgtc 1380
 ttacaatgtc attccccag 1400

<210> 44
 <211> 1334
 <212> DNA
 <213> HUMAN

<220>
 <221> intron
 <222> (1)..(1334)
 <223> 6th MN intron

<400> 44
 gtcagtttgt tggctctggcc actaatctct gtggcctagt tcataaagaa tcaccctttg 60
 gagcttcagg tctgaggctg gagatgggct ccctccagtg caggagggat tgaagcatga 120
 gccagcgctc atcttgataa taaccatgaa gctgacagac acagttaccc gcaaacggct 180
 gcctacagat tgaaaaccaa gcaaaaaccg cggggcacgg tggctcacgc ctgtaatccc 240
 agcacttttg gaggccaaagg caggtggatc acgagggtcaa gagatcaaga ccatcctggc 300
 caacatgggtg aaaccccatc tctactaaaa atacgaaaaa atagccaggc gtggtggcgg 360
 gtgcctgtaa tcccagctac tcgggaggct gaggcaggag aatggcatga acccgggagg 420
 cagaagttgc agtgagccga gatcgtgcc ctgcactcca gcctgggcaa cagagcgaga 480
 ctcttgtctc aaaaaaaaaa aaaaaaaga aaaccaagca aaaacaaaaa tgagacaaaa 540
 aaaacaagac caaaaaatgg tgtttggaaa ttgtcaaggc caagtctgga gagctaaact 600
 ttttctgaga actgtttatc ttttaataagc atcaaatatt ttaactttgt aaatactttt 660
 gttggaaatc gttctcttct tagtcactct tgggtcattt taaatctcac ttactctact 720
 agacctttta ggtttctgct agactaggta gaactctgcc tttgcatttc ttgtgtctgt 780
 tttgtatagt tatcaatatt catatttatt tacaagttat tcagatcatt ttttcttttc 840
 tttttttttt tttttttttt ttttacatct ttagtagaga cagggtttca ccatattggc 900
 caggctgctc tcaaactcct gaccttgtga tccaccagcc tcggcctccc aaagtgctgg 960
 gattcatttt ttctttttta tttgctctgg gcttaaactt gtggcccagc actttatgat 1020
 ggtacacaga gttaagagt tagactcaga cggctcttct tctttccttc tcttccttcc 1080
 tcccttcctc ccaccttcc cttctctcct tcctttcttt cttcctctct tgcttcctca 1140
 ggctcttccc agttgctcca aagccctgta cttttttttg agttaacgct ttatgggaag 1200
 ggctgcact tagtgaagaa gtggtctcag agttgagtta ccttggcttc tgggagggtga 1260
 aactgtatcc ctataccctg aagctttaag ggggtgcaat gtagatgaga cccaacata 1320
 gatcctcttc acag 1334

<210> 45
 <211> 512
 <212> DNA
 <213> HUMAN

<220>
 <221> intron
 <222> (1)..(512)
 <223> 7th MN intron

<400> 45

```
gtgggcctgg ggtgtgtgtg gacacagtgg gtgcggggga aagaggatgt aagatgagat 60
gagaaacagg agaagaaaga aatcaaggct gggctctgtg gcttacgcct ataatcccac 120
cacgttggga ggctgagggt ggagaatggg ttgagcccag gagttcaaga caaggcgggg 180
caacatagtg tgaccccatc tctacccaaa aaaccccaac aaaacccaaa atagccgggc 240
atggtggtat gcggcctagt cccagctact caaggaggct gaggtgggaa gatcgcttga 300
ttccaggagt ttgagactgc agtgagctat gatcccacca ctgcctacca tctttaggat 360
acatttattt atttataaaa gaaatcaaga ggctggatgg ggaatacagg agctggaggg 420
tggagccctg aggtgctggg tgtgagctgg cctgggacct ttgtttcctg tcatgccatg 480
aaccaccca cactgtccac tgacctccct ag 512
```

<210> 46

<211> 114

<212> DNA

<213> HUMAN

<220>

<221> intron

<222> (1)..(114)

<223> 8th MN intron

<400> 46

```
gtacagcttt gtctggtttc cccccagcca gtagtccctt atcctcccat gtgtgtgcca 60
gtgtctgtca ttggtgggtc cagcccgct ctcacatctc ctttttctct ccag 114
```

<210> 47

<211> 617

<212> DNA

<213> HUMAN

<220>

<221> intron

<222> (1)..(617)

<223> 9th MN intron

<400> 47

```
gtgagtctgc ccctcctctt ggtcctgatg ccaggagact cctcagcacc attcagcccc 60
agggtgctc .aggaccgct ctgctccctc tccttttctg cagaacagac cccaaccca 120
atattagaga ggcagatcat ggtggggatt ccccatctgt cccagaggc taattgatta 180
gaatgaagct tgagaaatct cccagcatcc ctctcgcaaa agaatcccc cccctttttt 240
taaagatagg gtctcactct gtttgcccca ggctgggggtg ttgtggcacg atcatagctc 300
actgcagcct cgaactccta ggctcaggca atcctttcac cttagcttct caaagcactg 360
ggactgtagg catgagccac tgtgcctggc cccaaacggc ccttttactt ggcttttagg 420
aagcaaaaac ggtgcttacc ttacctcttc tcgtgtatcc accctcatcc cttggctggc 480
```

```

ctcttctgga gactgaggca ctatggggct gcctgagAAC tcggggcagg ggtggtggag 540
tgactgagg caggtgttga ggaactctgc agaccctct tccttcccaa agcagccctc 600
tctgctctcc atcgag                                     617

```

```

<210> 48
<211> 130
<212> DNA
<213> HUMAN

```

```

<220>
<221> intron
<222> (1)..(130)
<223> 10th MN intron

```

```

<400> 48
gtattacact gaccctttct tcaggcACAA gcttccccca cccttgtgga gtcacttcat 60
gcaaagcgca tgcaaatgag ctgctcctgg gccagttttc tgattagcct ttctgtttgt 120
gtacacacag                                     130

```

```

<210> 49
<211> 1401
<212> DNA
<213> HUMAN

```

```

<400> 49
caaactttca cttttgttgc ccaggctgga gtgcaatggc gcgatctcgg ctcaactgcaa 60
cctccacctc ccgggttcaa gtgattctcc tgcctcagcc tctagccaag tagctgcgat 120
tacaggcatg cgccaccacg cccggctaatt ttttgtattt ttagtagaga cggggtttcg 180
ccatgtttggt caggctggtc tcgaactcct gatctcaggt gatccaacca ccctggcctc 240
ccaaagtgtc gggattatag gcgtgagcca cagcgctgg cctgaagcag ccactcactt 300
ttacagaccc taagacaatg attgcaagct ggtaggattg ctgtttggcc caccagctg 360
cgggtgttgag tttgggtgcg gtctcctgtg ctttgcacct ggcccgtta aggcatttgt 420
taccgtaat gtcctgtaa ggcattctcg tttgtgacat cgttttggtc gccaggaagg 480
gattggggct ctaagcttga gcggttcac cttttcattt atacagggga tgaccagagt 540
cattggcgct atggaggtga gacaccacc cgctgcacag acccaatctg ggaaccacgc 600
tctgtggatc tcccctacag ccgtccctga acaactggtc cgggcgtccc acccgccgcc 660
caccgtccca cccctcacc ttttctaccc ggggttccta agttcctgac ctaggcgtca 720
gacttctca ctatactctc ccaccccagg cgaccgccc tggccccggg tgtccccagc 780
ctgcgcgggc cgcttccagt ccccggtgga tatccgcccc cagctcgccg ccttctgccc 840
ggccctgcgc ccctggaac tcctgggctt ccagctcccg ccgctcccag aactgcgcct 900
gcgcaacaat ggccacagtg gtgagggggc ctccccgcgc agacttgggg atggggcggg 960
gcgcagggaa gggaaccgtc gcgcagtgcc tgcccggggg ttgggctggc cctaccgggc 1020
ggggccggct cacttgctc tcctacgca gtgcaactga ccctgcctcc tgggctagag 1080
atggctctgg gtcccgggcg ggagtaccgg gctctgcagc tgcattctgca ctggggggct 1140

```

gcaggtcgtc cgggctcgga gcacactgtg gaaggccacc gtttccctgc cgaggtgagc 1200
gcggactggc cgagaagggg caaaggagcg gggcggacgg gggccagaga cgtggccctc 1260
tcctaccctc gtgtcctttt cagatccacg tgggtcacct cagcaccgcc tttgccagag 1320
ttgacgaggc cttggggcgc ccgggaggcc tggccgtgtt ggccgccttt ctggaggtac 1380
cagatcctgg acacccccta c 1401

<210> 50
<211> 59
<212> PRT
<213> HUMAN

<400> 50
Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu
1 5 10 15
Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro
20 25 30
Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro
35 40 45
Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
50 55

<210> 51
<211> 257
<212> PRT
<213> HUMAN

<400> 51
Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp Pro
1 5 10 15
Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp Ile
20 25 30
Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu
35 40 45
Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn
50 55 60
Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu
65 70 75 80

Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp	Gly			
				85					90					95				
Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	Phe			
			100					105					110					
Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	Val			
		115					120					125						
Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala	Phe			
	130					135					140							
Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Gln	Leu	Leu	Ser			
145					150					155					160			
Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	Glu	Thr	Gln	Val	Pro	Gly			
				165					170					175				
Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe	Ser	Arg	Tyr	Phe	Gln			
			180					185					190					
Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala	Gln	Gly	Val	Ile	Trp			
		195					200					205						
Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala	Lys	Gln	Leu	His	Thr			
	210					215					220							
Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	Asn			
225					230					235					240			
Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	Phe			
				245					250					255				

Pro

<210> 52

<211> 20

<212> PRT

<213> HUMAN

<400> 52

Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu	Leu	Phe	Ala	Val	Thr	Ser	Val	Ala
1				5					10					15	

Phe Leu Val Gln
20

<210> 53
<211> 25
<212> PRT
<213> HUMAN

<400> 53
Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
1 5 10 15

Pro Ala Glu Val Ala Glu Thr Gly Ala
20 25

<210> 54
<211> 59
<212> PRT
<213> HUMAN

<400> 54
Ser Ala Ser Glu Glu Pro Ser Pro Ser Glu Val Pro Phe Pro Ser Glu
1 5 10 15

Glu Pro Ser Pro Ser Glu Glu Pro Phe Pro Ser Val Arg Pro Phe Pro
20 25 30

Ser Val Val Leu Phe Pro Ser Glu Glu Pro Phe Pro Ser Lys Glu Pro
35 40 45

Ser Pro Ser Glu Glu Pro Ser Ala Ser Glu Glu
50 55

<210> 55
<211> 470
<212> RNA
<213> HUMAN

<400> 55
cauggccccg auaaccuucu gccugugcac acaccugccc cucacuccac ccccauccua 60
gcuuugguau gggggagagg gcacagggcc agacaaaccu gugagacuuu ggcuccaucu 120
cugcaaaagg ggcucugug agucagccug cucccccucca ggcuugcucc uccccaccc 180
agcucucguu uccaugcac guacagcccg uacacaccgu gugcuggggac accccacagu 240

```

cagccgcaug gcuccccugu gcccagccc cuggcuccu cuguugauc cggcccccugc 300
uccagggcuc acugugcaac ugcugcuguc acugcugcu cuggugccug uccaucacca 360
gagguugccc cggaugcagg aggaucccc cuugggagga ggcucuucug gggaagauga 420
cccacugggc gaggaggauc ugcccaguga agaggauca cccagagagg 470

```

```

<210> 56
<211> 292
<212> DNA
<213> HUMAN

```

```

<400> 56
gttttttttga gacggagtct tgcattctgtc atgcccaggc tggagtagca gtggtgccat 60
ctcggctcac tgcaagctcc acctcccgag ttcacgcat tttcctgcct cagcctcccg 120
agtagctggg actacaggcg cccgccacca tgcccggcta attttttgta tttttggtag 180
agacgggggtt tcaccgtgtt agccagaatg gtctcgatct cctgacttcg tgatccaccc 240
gcctcggcct cccaaagtct tgggattaca ggtgtgagcc accgcacctg gc 292

```

```

<210> 57
<211> 262
<212> DNA
<213> HUMAN

```

```

<400> 57
tttttttttt gagacagggt cttgctctgt caccagggc agagtgcaat ggtacagtct 60
cagctcactg cagcctcaac cgctcggct caaacatca tccatttca gcctcctgag 120
tagctgggac tacaggcaca tgccattaca cctggcta atttttgtat ttctagtaga 180
gacaggggtt ggccatgttg cccgggctgg tctcgaactc ctggactcaa gcaatccacc 240
cacctcagcc tcccaaatg ag 262

```

```

<210> 58
<211> 2501
<212> DNA
<213> HUMAN

```

```

<220>
<221> misc_feature
<222> (1)..(2501)
<223> region 5' to transcription initiation site as determined by
RNase protection assay (nucleotide 3507 of Figures 2A-2F and
of SEQ ID NO: 5), corresponding to region of SEQ ID NO: 5
and Figures 2A-2F from nucleotide (7) to nucleotide (2507),
in which region some regulatory elements are probably situated.

```

<220>

<221> unsure what base is at position 1968

<222> (1968)

<223> unsure of base at position 1968, which is the same unknown base as that at position 1974 of SEQ ID NO. 5, i.e., the full-length MN genomic sequence, and of that unknown at position 1968 of SEQ ID NO: 90, and unknown at position 647 of SEQ ID NO: 110. That unknown base is in the 5' region flanking the transcription initiation site (3507) as determined by RNase protection assay.

<400> 58

```
tgttgactcg tgaccttacc cccaaccctg tgcctctctga aacatgagct gtgtccactc 60
agggttaaatt ggattaaggcg cgggtgcaaga tgtgcttttgt taaacagatg cttgaaggca 120
gcatgctcgt taagagtcac caccaatccc taatctcaag taatcaggga cacaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgacct tgccaaatcc cctctgtga gaaacaccca 300
agaattatca ataaaaaaat aaatttataa aaaaaatata aaaaaaaaaa aaaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaagtat 420
catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480
cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc cccaagtctc 540
taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600
ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaattttaa 660
ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaatt tttgtagtta 720
atggatgcac tgtgaatctt gctatgatag ttttcctcca cactttgcca ctaggggtag 780
gtaggtactc agttttcagt aattgcttac ctaagacctt aagccctatt tctcttgtag 840
tggcctttat ctgtaatatg ggcataattt atacaatata atttttggag tttttttgtt 900
tgtttgtttg tttgtttttt tgagacggag tcttgcatct gtcatgccca ggctggagta 960
gcagtgggtg catctcggct cactgcaagc tccacctccc gagttcacgc cattttcctg 1020
cctcagcctc ccgagtagct gggactacag gcgcccgcga ccatgcccgg ctaatttttt 1080
gtattttttg tagagacggg gtttcaccgt gttagccaga atggtctcga tctcctgact 1140
tcgtgatcca ccgcctcgg cctcccaaag ttctgggatt acaggtgtga gccaccgcac 1200
ctggccaatt ttttgagctt tttaaagtaa aaatatgtct tgtaagctgg taactatggg 1260
acatttcctt ttattaatgt ggtgctgacg gtcataatag ttcttttgag tttggcatgc 1320
atatgctact ttttgagctt ctttcattac atttttctct cttcatttga agagcatggt 1380
atatctttta gcttcacttg gcttaaaagg ttctctcatt agcctaacac agtgtcattg 1440
ttggtaccac ttggatcata agtggaaaaa cagtcaagaa attgcacagt aatacttggt 1500
tgtaagaggg atgattcagg tgaatctgac actaagaaac tcccctacct gaggtctgag 1560
attcctctga cattgctgta tataggcttt tcctttgaca gctgtgact gcggactatt 1620
tttcttaagc aagatatgct aaagttttgt gagccttttt ccagagagag gtctcatatc 1680
tgcacaaagt gagaacatat aatgtctgca tgtttccata tttcaggaat gtttgcttgt 1740
gttttatgct tttatataga cagggaact tggtcctcag tgacccaaaa gaggtgggaa 1800
ttgttattgg atatcatcat tggcccacgc tttctgacct tggaaacaat taagggttca 1860
taatctcaat tctgtcagaa ttggtacaag aaatagctgc tatgtttctt gacattccac 1920
ttggtaggaa ataagaatgt gaaactcttc agttggtgtg tgtccctngt ttttttgcaa 1980
tttccttctt actgtgttaa aaaaaagtat gatcttgctc tgagaggtga ggcattctta 2040
atcatgatct ttaaagatca ataataaat cctttcaagg attatgtctt tattataata 2100
```

```

aagataattt gtctttaaca gaatcaataa tataatccct taaaggatta tatctttgct 2160
gggcgcagtg gctcacacct gtaatcccag cactttgggt ggccaagggt gaaggatcaa 2220
atctgcctac ttctatatta tcttctaaag cagaattcat ctctcttccc tcaatatgat 2280
gatattgaca gggtttgccc tcaactcacta gattgtgagc tcctgctcag ggcaggtagc 2340
gtttttttgtt tttgtttttg tttttctttt ttgagacagg gtcttgctct gtcaccacagg 2400
ccagagtgca atggtacagt ctcagctcac tgcagcctca accgcctcgg ctcaaaccat 2460
catcccatth cagcctcctg agtagctggg actacaggca c 2501

```

<210> 59

<211> 292

<212> DNA

<213> HUMAN

<220>

<221> misc_feature

<222> (1)

<400> 59

```

ttttttttgag acggagtctt gcctctgtca tgcccagggt ggagtagcag tgggtgccatc 60
tcggctcact gcaagctcca cctcccaggt tcacgccatt ttctgcctc agcctcccga 120
gtagctggga ctacaggcgc ccgccaccat gcccggttaa ttttttgtat ttttggtaga 180
gacgggggtt caccgtgtta gccagaatgg tctcgatctc ctgacttcgt gatccaccg 240
cctcggcctc ccaaagtctt gggattacag gtgtgagcca ccgcacctgg cc 292

```

<210> 60

<211> 262

<212> DNA

<213> HUMAN

<400> 60

```

ttctttttttg agacagggtc ttgctctgtc acccaggcca gagtgcaatg gtacagtctc 60
agctcactgc agcctcaacc gcctcggctc aaaccatcat ccatttcag cctcctgagt 120
agctgggact acaggcacat gccattacac ctggctaatt tttttgtatt tctagtagag 180
acagggtttg gccatgttgc ccgggctggg ctcgaaactc tggactcaag caatccaccc 240
acctcagcct cccaaaatga gg 262

```

<210> 61

<211> 294

<212> DNA

<213> HUMAN

<400> 61

```

ttttttttttg agacaaactt tcacttttgt tgcccagggt ggagtgcaat ggcgcgatct 60

```


cggtcactg	caacctccac	ctcccgggtt	caagtgattc	tctgcctca	gcctctagcc	120
aagtagctgc	gattacaggc	atgcgccacc	acgcccggct	aatttttgta	tttttagtag	180
agacgggggtt	tcgccatgtt	ggtcaggctg	gtctcgaact	cctgatctca	ggatgatccaa	240
ccaccctggc	ctcccaaagt	gctgggatta	taggcgtgag	ccacagcgcc	tggc	294

<210> 62

<211> 276

<212> DNA

<213> HUMAN

<400> 62

tgacagtctc	tctgtcgccc	aggctggagt	gcagtgggtg	gatcttgggt	cactgcaact	60
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gtgtgtgcca	ccatgcccag	ctaatttttt	tttgtatttt	tagtagacag	ggtttcacca	180
tgttggtcag	gctgggtctca	aactcctggc	ctcaagtgat	ccgcctgact	cagcctacca	240
aagtgctgat	tacaagtgtg	agccaccgtg	cccagc			276

<210> 63

<211> 289

<212> DNA

<213> HUMAN

<400> 63

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aaatacgaaa	aatagccag	gcgtgggtggc	gggtgcctgt	aatcccagct	actcggggagg	180
ctgaggcagg	agaatggcat	gaacccggga	ggcagaagtt	gcagtgagcc	gagatcgtgc	240
cactgcactc	cagcctgggc	aacagagcga	gactcttgtc	tcaaaaaaa		289

<210> 64

<211> 298

<212> DNA

<213> HUMAN

<400> 64

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caaaaaaacc	ccaacaaaac	caaaaatagc	cgggcatggt	ggtatgcggc	ctagtcccag	180
ctactcaagg	aggctgaggt	gggaagatcg	cttgattcca	ggagtgtgag	actgcagtga	240
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<210> 65

<211> 105
<212> DNA
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<400> 65
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ctgaccttgt gatccaccag cctcggcctc ccaaagtgt gggat 105

<210> 66
<211> 83
<212> DNA
<213> HUMAN

<400> 66
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aggcatgagc cactgtgcct ggc 83

<210> 67
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<212> DNA
<213> HUMAN

<400> 67
agaaggtaag t 11

<210> 68
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<212> DNA
<213> HUMAN

<400> 68
tggaggtgag a 11

<210> 69
<211> 11
<212> DNA
<213> HUMAN

<400> 69
cagtcgtgag g 11

<210> 70
<211> 11
<212> DNA
<213> HUMAN

<400> 70
ccgaggtgag c 11

<210> 71
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<212> DNA
<213> HUMAN

<400> 71
tggaggtacc a 11

<210> 72
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<213> HUMAN

<400> 72
ggaaggtcag t 11

<210> 73
<211> 11
<212> DNA
<213> HUMAN

<400> 73
agcaggtggg c 11

<210> 74
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<400> 74
gccaggtaca g 11

<210> 75

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<400> 75
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atacagggga t 11

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<400> 77
atacagggga t 11

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<400> 78
ccccaggcga c 11

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<400> 79
acgcagtgca a 11

<210> 80
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<400> 80
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<400> 81
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<400> 83
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<400> 84
ctccagtcca g 11

<210> 85
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<212> DNA

<213> HUMAN

<400> 85

tcgcaggtga ca

12

<210> 86

<211> 11

<212> DNA

<213> HUMAN

<400> 86

acacagaagg g

11

<210> 87

<211> 377

<212> PRT

<213> HUMAN

<400> 87

Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly Ser

1 5 10 15

Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu

20 25 30

Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly

35 40 45

Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys

50 55 60

Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu

65 70 75 80

Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys

85 90 95

Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp

100 105 110

Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp

115 120 125

Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu	130	135	140	
Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn	145	150	155	160
Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala	165	170	175	
Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp	180	185	190	
Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	195	200	205	
Phe	Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	210	215	220	
Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala	225	230	235	240
Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Gln	Leu	Leu	245	250	255	
Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	Glu	Thr	Gln	Val	Pro	260	265	270	
Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe	Ser	Arg	Tyr	Phe	275	280	285	
Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala	Gln	Gly	Val	Ile	290	295	300	
Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala	Lys	Gln	Leu	His	305	310	315	320
Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	325	330	335	
Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	340	345	350	
Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln	355	360	365	

Leu Asn Ser Cys Leu Ala Ala Gly Asp
370 375

<210> 88
<211> 34
<212> DNA
<213> HUMAN

<400> 88
tagacagatc tacgatggct cccctgtgcc ccag 34

<210> 89
<211> 34
<212> DNA
<213> HUMAN

<400> 89
attcctctag acagttaccg gctccccctc agat 34

<210> 90
<211> 3532
<212> DNA
<213> HUMAN

<220>
<221> misc_feature which includes the MN gene promoter
<222> (1)..(3532)
<223> region including the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter, and corresponds to nucleotide 7 to nucleotide 3538 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of the base at position 1968, which is the same unknown base at position 1974 of SEQ ID NO: 5 (the full-length MN genomic sequence), position 1968 of SEQ ID NO: 58 and position 647 of SEQ ID NO: 110. That unknown base is in the region that includes the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase

protection assay, which region is inclusive of the MN gene promoter.

<400> 90

tggtgactcg	tgaccttacc	cccaaccctg	tgctctctga	aacatgagct	gtgtccactc	60
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gcatgctcgt	taagagtc	caccaatccc	taatctcaag	taatcaggga	cacaaacact	180
gcggaaggcc	gcagggctcct	ctgcctagga	aaaccagaga	cctttgttca	cttgtttatc	240
tgaccttccc	tccactattg	tccatgaccc	tgccaaatcc	ccctctgtga	gaaacaccca	300
agaattatca	ataaaaaaat	aaatttataa	aaaaaataca	aaaaaaaaaa	aaaaaaaaaa	360
aaaagactta	cgaatagtta	ttgataaatg	aatagctatt	ggtaaagcca	agtaa	420
catattcaaa	accagacggc	catcatcaca	gctcaagtct	acctgatttg	atctctttat	480
cattgtcatt	ctttggattc	actagattag	tcatcatcct	caaaattctc	ccccaagttc	540
taattacgtt	ccaacattt	aggggttaca	tgaagcttga	acctactacc	ttctttgctt	600
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gtatttttgg	tagagacggg	gtttcacctg	gttagccaga	atggctctga	tctcctgact	1140
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aagataaatt	gtctttaaca	gaatcaataa	tataatccct	taaaggatta	tatctttgct	2160
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<210> 91
 <211> 204
 <212> DNA
 <213> HUMAN

<400> 91	
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ccctccaggc	ttgctcctcc cccaccagc tctcgtttcc aatgcacgta cagcccgtac 180
acaccgtgtg	ctgggacacc ccac 204

<210> 92
 <211> 132
 <212> DNA
 <213> HUMAN

<400> 92	
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aaggcagcat	gc 132

<210> 93
 <211> 275
 <212> DNA
 <213> HUMAN

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acagcccgtgta cacaccgtgt gctgggacac cccac 275

<210> 94
<211> 89
<212> DNA
<213> HUMAN

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ccgtacacac cgtgtgctgg gacacccc a 89

<210> 95
<211> 61
<212> DNA
<213> HUMAN

<400> 95
caccagctc tcgtttccaa tgcacgtaca gcccgtagac accgtgtgct gggacacccc 60
a 61

<210> 96
<211> 116
<212> DNA
<213> HUMAN

<400> 96
acctgcccct cactccaccc ccatacctagc tttggtatgg gggagagggc acagggccag 60
acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcc 116

<210> 97
<211> 36
<212> PRT
<213> HUMAN

<400> 97
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Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu
20 25 30

Glu Asp Leu Pro
35

<210> 98
<211> 6
<212> PRT
<213> HUMAN

<400> 98
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1 5

<210> 99
<211> 4
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1 5

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1 5

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<400> 102
Glu Glu Asp Leu Pro Ser Glu
1 5

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Asp Leu Pro Gly Glu Glu
1 5

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Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro
1 5 10 15
Ser Glu Glu Asp Ser Pro
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<210> 105
<211> 25
<212> PRT
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1 5 10 15
Pro Pro Gly Glu Glu Asp Leu Pro Gly
20 25

<210> 106
<211> 24
<212> PRT
<213> HUMAN

<400> 106
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1 5 10 15

Gly Glu Glu Asp Leu Pro Glu Val
20

<210> 107
<211> 7
<212> PRT
<213> HUMAN

<400> 107
Gly Glu Thr Arg Ala Pro Leu
1 5

<210> 108
<211> 7
<212> PRT
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<400> 108
Gly Glu Thr Arg Glu Pro Leu
1 5

<210> 109
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<400> 109
Gly Gln Thr Arg Ser Pro Leu
1 5

<210> 110
<211> 1247
<212> DNA

<213> HUMAN

<220>

<221> misc_feature

<222> (1)..(1247)

<223> region 5' to the transcription initiation site as determined by RNase protection assay (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) in which an activating element is localized, which region corresponds to nucleotide 1328 to nucleotide 2574 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>

<221> unsure what base is at position 647

<222> (647)

<223> unsure of the base at position 647, which is the same unknown base as that at position 1974 of SEQ ID NO: 5, and as that at position 1968 of SEQ ID NOS: 58 and 90. That unknown base at position 647 is in a region in which an activating element is localized and is 5' to the transcription initiation site.

<400> 110

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gtaagagggg tgattcaggt gaatctgaca ctaagaaact cccctacctg aggtctgaga 240
ttcctctgac attgctgtat ataggctttt cctttgacag cctgtgactg cggactattt 300
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gcatcaagtg agaacatata atgtctgcat gtttccatat ttcaggaatg tttgcttgtg 420
ttttatgctt ttatatagac agggaaactt gttcctcagt gacccaaaag aggtgggaat 480
tgttattgga tatcatcatt ggcccacgct ttctgacctt ggaaacaatt aagggttcat 540
aatctcaatt ctgtcagaat tggtacaaga aatagctgct atgtttcttg acattccact 600
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ttccttctta ctgtgttaaa aaaaagtatg atcttgctct gagaggtgag gcattcttaa 720
tcatgatctt taaagatcaa taatataatc ctttcaagga ttatgtcttt attataataa 780
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atcccatttc agcctcctga gtagctggga ctacaggcac atgccattac acctgggctaa 1200
tttttttgta tttctagtag agacagggtt tggccatggt gcccggg 1247
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<210> 111

<211> 17

<212> DNA
 <213> HUMAN

 <400> 111
 ctctgtgagt cagcctg 17

 <210> 112
 <211> 23
 <212> DNA
 <213> HUMAN

 <400> 112
 aggcttgctc ctccccacc cag 23

 <210> 113
 <211> 18
 <212> DNA
 <213> HUMAN

 <400> 113
 agactttggc tccatctc 18

 <210> 114
 <211> 20
 <212> DNA
 <213> HUMAN

 <400> 114
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 <210> 115
 <211> 26
 <212> DNA
 <213> HUMAN

 <400> 115
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 <210> 116
 <211> 20
 <212> PRT

<213> HUMAN

<400> 116

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1 5 10 15

Gly Gly Gly Ser
20

<210> 117

<211> 34

<212> DNA

<213> HUMAN

<400> 117

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<210> 118

<211> 15

<212> PRT

<213> HUMAN

<400> 118

Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
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